```
                        GenCore version 5.1.3
                   Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        February 21, 2003, 12:30:13 ; Search time 92 Seconds
                                            (without alignments)
                                            4.479 Million cell updates/sec

Title:          SHORT-PEP
Perfect score:  16
Sequence:       1 rw 2

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:    4

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

Database :      SPTREMBL_21:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
               10:  sp_plant:*
               11:  sp_rodent:*
               12:  sp_virus:*
               13:  sp_vertebrate:*
               14:  sp_unclassified:*
               15:  sp_rvirus:*
               16:  sp_bacteriap:*
               17:  sp_archeap:*

                Pred. No. is the number of results predicted by chance to have a
                score greater than or equal to the score of the result being printed,
                and is derived by analysis of the total score distribution.

                                        SUMMARIES

Result                  %    Query
No.     Score   Match  Length  DB  ID        Description
------  -----   -----  ------  --  --------   -----------
  1       6     37.5     5     13  P83308     P83308 gallus gall
  2       2     12.5     4     11  Q08433     Q08433 rattus norv
  3       2     12.5     5      2  P83073     P83073 bacillus ce
  4       2     12.5     5     10  Q99007     Q99007 hordeum vul

                                       ALIGNMENTS

RESULT 1
P83308
ID    P83308
AC    P83308;
DT    01-JUN-2002 (TrEMBLrel. 21, Created)
DT    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE    FMRFamide-like neuropeptide (LPLRF-amide).
OS    Gallus gallus (Chicken).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC    Gallus.
OX    NCBI_TaxID=9031;
RN    [1]
RP    SEQUENCE, AND SYNTHESIS.
RC    TISSUE=BRAIN;
RX    PubMed=6137771;
RA    Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT    "A novel active pentapeptide from chicken brain identified by
RT    antibodies to FMRFamide.";
RL    Nature 305:328-330(1983).
CC    -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC    -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC        FAMILY.
KW    Neuropeptide.
SQ    SEQUENCE    5 AA;   645 MW;  69D40737674000000 CRC64;

Query Match           37.5%;  Score 6;  DB 13;  Length 5;
Best Local Similarity 50.0%;  Pred. No. 6.7e+05;
Matches   1; Conservative   1; Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 RW 2
            |:
Db      4 RF 5

RESULT 2
Q08433
ID    Q08433         PRELIMINARY;          PRT;      4 AA.
AC    Q08433;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT    01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE    UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
DE    (Fragment).
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX    NCBI_TaxID=10116;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=GUNN;
RX    MEDLINE=91282758; PubMed=1840486;
RA    Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT    "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT    hyperbilirubinemic Gunn rat.";
RL    Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC    -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC        SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC        ENDOGENOUS COMPOUNDS.
CC    -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC        BETA-D-GLUCORONOSIDE.
CC    -!- SUBCELLULAR LOCATION: MICROSOME.
DR    EMBL; S38636; AAB19259.1; -.
KW    Transferase; Glycosyltransferase; Microsome; Multigene family.
FT    NON_TER          1          1
FT    NON_TER          4          4
SQ    SEQUENCE    4 AA;   473 MW;  637332642000000000 CRC64;

Query Match           12.5%;     Score 2;  DB 11;  Length 4;
Best Local Similarity  0.0%;  Pred. No. 6.7e+05;
Matches   0; Conservative   1; Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 R 1
            :
Db      4 K 4

RESULT 3
P83073
```

```
ID   P83073;      PRELIMINARY;   PRT;    5 AA.
AC   P83073;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   88 kDa protein (Fragment).
OS   Bacillus cereus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Bacillaceae; Bacillus.
OX   NCBI_TaxID=1396;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=NCIMB 11796;
RA   Browne N., Dowds B.C.A.;
RL   Submitted (JUL-2001) to the SWISS-PROT data bank.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  623 MW;  6B01AAA336F00000 CRC64;
```

```
Query Match             12.5%;  Score 2;  DB 2;  Length 5;
  Best Local Similarity   0.0%;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 R 1
              .
Db          2 K 2
```

```
RESULT 4
ID   Q99007      PRELIMINARY;   PRT;    5 AA.
AC   Q99007;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Alpha-amylase (EC 3.2.1.1) (Fragment).
GN   AMY1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX   MEDLINE=91329704; PubMed=1831055;
RA   Jacobsen J.V., Close T.J.;
RT   "Control of transient expression of chimaeric genes by gibberellic
RT   acid and abscisic acid in protoplasts prepared from mature barley
RT   aleurone layers.";
RL   Plant Mol. Biol. 16:713-721(1991).
CC   -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC       LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC       BARLEY.
DR   EMBL; X54643; CAA38455.1; -.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW   Calcium; Multigene family.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  600 MW;  61E33443DD6F00000 CRC64;
```

```
Query Match             12.5%;  Score 2;  DB 10;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 6.7e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 R 1
              .
Db          4 K 4
```

Search completed: February 21, 2003, 12:33:48
Job time : 93 secs